Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A method of detecting and analyzing differences between nucleic acids from two sources, which method comprises:

a. providing the nucleic acids from two sources as labeled probes wherein the nucleic acids from ~~two sources~~ each source are labeled with ~~two different markers~~ a distinct marker;

b. forming a mixture of the labeled probes with pooled reagents of at least two reagents wherein each of the pooled reagents comprises a population of beads carrying a polynucleotide target of known sequence, the polynucleotide target of any one of the pooled reagents being different from the target of any other of the pooled reagents and the beads of any one of the pooled reagents being distinguishable from the beads of any other of the pooled reagents by flow cytometry;

c. incubating the mixture under conditions to promote specific hybridization between probes and targets; and

d. analyzing beads in the mixture by flow cytometry to determine the identity of each bead and to quantify the relative abundance of each target sequence in the two sources.

Claim 2 (original): The method of claim 1 wherein the nucleic acids from two sources are mRNA or cDNA from cells or tissues.

Claim 3 (previously presented): The method of claim 1 wherein the polynucleotide targets are cDNA derived from cellular mRNA.

Claim 4 (previously presented): The method of claim 1 wherein the polynucleotide targets are PCR amplimers.

Claim 5 (previously presented): The method of claim 1 wherein the polynucleotide targets contain terminal biotin groups through which they are attached to streptavidin-coated beads.

Claim 6 (previously presented): The method of claim 1 wherein the polynucleotide targets are single-stranded nucleic acids.

Claim 7 (previously presented): The method of claim 1 wherein the nucleic acids are single-stranded nucleic acids.

Claim 8 (previously presented): The method of claim 1 wherein beads of one pooled reagent are distinguishable from beads of another pooled reagent by size.

Claim 9 (previously presented): The method of claim 1 wherein beads of one pooled reagent are distinguishable from beads of another pooled reagent by the nature of one or more markers attached to the beads.

Claim 10 (previously presented): The method of claim 1 wherein beads of one pooled reagent are distinguishable from beads of another pooled reagent by the concentration of one or more markers attached to the beads.

Claim 11 (previously presented): The method of claim 1 wherein beads of one pooled reagent are distinguishable from beads of another pooled reagent by the size and/or by the nature and the concentration of one or more markers attached to the beads.

Claim 12 (previously presented): The method of claim 9 wherein the markers are fluorescent markers attached to the beads.

Claim 13 (previously presented): The method of claim1 wherein each of the nucleic acids is labelled with a fluorescent tag to indicate its source.

Claim 14 (cancelled)

Claim 15 (previously presented): The method of claim 1 further comprising the step of analysing the data obtained by flow cytometry to yield information about the relative and/or absolute abundances of individual nucleic acid sequences contained within the nucleic acids from two sources.

Claim 16 (previously presented): The method of claim 10 wherein the markers are fluorescent markers attached to the beads.

Claim 17 (previously presented): The method of claim 11 wherein the markers are fluorescent markers attached to the beads.